

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/539,105

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the **only valid** <213> responses are: Unknown, Artificial Sequence or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or Artificial Sequence

11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" **can only represent a single nucleotide**; "Xaa" **can only represent a single amino acid**



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005
TIME: 11:17:05

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272005\J539105.raw

5 <110> APPLICANT: Garvan Institute of Medical Research
9 <120> TITLE OF INVENTION: Methods of treatment of feeding disorders or disorders of glucose uptake
10 and for modifying metabolism and identifying therapeutic reagents therefor
14 <130> FILE REFERENCE: 502008/MRO
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/539,105
C--> 18 <141> CURRENT FILING DATE: 2005-06-15
18 <150> PRIOR APPLICATION NUMBER: AU 2002953393
20 <151> PRIOR FILING DATE: 2002-12-16
24 <150> PRIOR APPLICATION NUMBER: AU 2003906285
26 <151> PRIOR FILING DATE: 2003-11-14
30 <160> NUMBER OF SEQ ID NOS: 261
34 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

4948 <210> SEQ ID NO: 251
4950 <211> LENGTH: 2721
4952 <212> TYPE: DNA
4954 <213> ORGANISM: c-Cbl Y700F
4958 <220> FEATURE:
4960 <221> NAME/KEY: CDS
4962 <222> LOCATION: (1)..(2718)
4964 <223> OTHER INFORMATION:
W--> 4968 <400> 251
4969 atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc acg ggc
4970 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Thr Gly
4971 1 5 10 15
4973 tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc
4974 Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala
4975 20 25 30
4977 ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg
4978 Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro
4979 35 40 45
4981 ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac
4982 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
4983 50 insert space 55 60 more over
E--> 4985 aag ctg gtg cgg ggt cag aac cca aag ctg ggc cta aag aat agc
W--> 4986 Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
4987 65 70 75 80
E--> 4989 cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt
4990 Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
4991 85 90 95

Does Not Comply
Corrected Diskette Needed
(pg. 1-5)

Found 2719
INVALID
Response
<213> response has
to be either Artificial,
Unknown or Genus/
Species.
See item
#10 on
error
summary
sheet.

240 - 238

288 - 286

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Input Set : A:\PTO.RJ.txt
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E--> 4993 act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat
4994 Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
4995 100 105 110
E--> 4997 gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa
4998 Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
4999 115 120 125
E--> 5001 acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat
5002 Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
5003 130 135 140
E--> 5005 tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac
5006 Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
5007 145 150 155 160
E--> 5009 atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga
5010 Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
5011 165 170 175
E--> 5013 gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa
5014 Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
5015 180 185 190
E--> 5017 gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct
5018 Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
5019 195 200 205
E--> 5021 cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg
5022 Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
5023 210 215 220
E--> 5025 aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa
5026 Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
5027 225 230 235 240
E--> 5029 ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg
5030 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
5031 245 250 255
E--> 5033 aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg
5034 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
5035 260 265 270
E--> 5037 acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct
5038 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
5039 275 280 285
E--> 5041 ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct
5042 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
5043 290 295 300
E--> 5045 att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac
5046 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
5047 305 310 315 320
E--> 5049 aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc
5050 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
5051 325 330 335
E--> 5053 tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta
5054 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
5055 340 345 350
E--> 5057 tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat

336-334
384-382
432-430
480-479
528-526
576-574
624-622
672-670
720-718
768-766
816-814
864-862
912-910
960-958
1008-1006
1056-1054
1104-1102

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5058	Cys	Glu	Pro	Thr	Pro	Gln	Asp	His	Ile	Lys	Val	Thr	Gln	Gln	Tyr			
5059				355					360				365					
E-->	5061	gaa	tta	tac	tgt	gag	atg	ggc	tcc	aca	ttc	caa	cta	tgt	aaa	ata	tgt	1152
5062	Glu	Leu	Tyr	Cys	Glu	Met	Gly	Ser	Thr	Phe	Gln	Leu	Cys	Lys	Ile	Cys		
5063					370				375			380						
E-->	5065	gct	gaa	aat	gat	aag	gat	gta	aag	att	gag	ccc	tgt	gga	cac	ctc	atg	1200
5066	Ala	Glu	Asn	Asp	Lys	Asp	Val	Lys	Ile	Glu	Pro	Cys	Gly	His	Leu	Met		
5067	385					390				395			400					
E-->	5069	tgc	aca	tcc	tgt	ctt	aca	tcc	tgg	cag	gaa	tca	gaa	ggt	cag	ggc	tgt	1248
5070	Cys	Thr	Ser	Cys	Leu	Thr	Ser	Trp	Gln	Glu	Ser	Glu	Gly	Gln	Gly	Cys		
5071						405				410			415					
E-->	5073	cct	ttc	tgc	cga	tgt	gaa	att	aaa	ggt	act	gaa	ccc	atc	gtg	gta	gat	1296
5074	Pro	Phe	Cys	Arg	Cys	Glu	Ile	Lys	Gly	Thr	Glu	Pro	Ile	Val	Val	Asp		
5075						420				425			430					
E-->	5077	ccg	ttt	gat	cct	aga	ggg	agt	ggc	agc	ctg	ttg	agg	caa	gga	gca	gag	1344
5078	Pro	Phe	Asp	Pro	Arg	Gly	Ser	Gly	Ser	Leu	Leu	Arg	Gln	Gly	Ala	Glu		
5079						435				440			445					
E-->	5081	gga	gct	ccc	tcc	cca	aat	tat	gat	gat	gat	gat	gaa	cga	gct	gat		1392
5082	Gly	Ala	Pro	Ser	Pro	Asn	Tyr	Asp	Asp	Asp	Asp	Asp	Asp	Glu	Arg	Ala	Asp	
5083						450				455			460					
E-->	5085	gat	act	ctc	ttc	atg	atg	aag	gaa	ttg	gct	ggt	gcc	aag	gtg	gaa	cg	1440
5086	Asp	Thr	Leu	Phe	Met	Met	Lys	Glu	Leu	Ala	Gly	Ala	Lys	Val	Glu	Arg		
5087						465				470			475			480		
E-->	5089	ccg	cct	tct	cca	ttc	tcc	atg	gcc	cca	caa	gct	tcc	ctt	ccc	ccg	gt	1488
5090	Pro	Pro	Ser	Pro	Phe	Ser	Met	Ala	Pro	Gln	Ala	Ser	Leu	Pro	Pro	Val		
5091						485				490			495					
E-->	5093	cca	cca	cga	ctt	gac	ctt	ctg	ccg	cag	cga	gta	tgt	gtt	ccc	tca	agt	1536
5094	Pro	Pro	Arg	Leu	Asp	Leu	Leu	Pro	Gln	Arg	Val	Cys	Val	Pro	Ser	Ser		
5095						500				505			510					
E-->	5097	gct	tct	gct	ttt	gga	act	gct	tct	aag	gct	gct	tct	ggc	tcc	ctt	cat	1584
5098	Ala	Ser	Ala	Leu	Gly	Thr	Ala	Ser	Lys	Ala	Ala	Ser	Gly	Ser	Leu	His		
5099						515				520			525					
E-->	5101	aaa	gac	aaa	cca	ttt	cca	gta	cct	ccc	aca	ctt	cga	gat	ctt	cca	cca	1632
5102	Lys	Asp	Lys	Pro	Leu	Pro	Val	Pro	Pro	Thr	Leu	Arg	Asp	Leu	Pro	Pro		
5103						530				535			540					
E-->	5105	cca	ccg	cct	cca	gac	cg	cca	tat	tct	gtt	gga	gca	gaa	tcc	cga	cct	1680
5106	Pro	Pro	Pro	Pro	Asp	Arg	Pro	Tyr	Ser	Val	Gly	Ala	Glu	Ser	Arg	Pro		
5107						545				550			555			560		
E-->	5109	caa	aga	cgc	ccc	ttt	cct	tgt	aca	cca	ggc	gac	tgt	ccc	tcc	aga	gac	1728
5110	Gln	Arg	Arg	Pro	Leu	Pro	Cys	Thr	Pro	Gly	Asp	Cys	Pro	Ser	Arg	Asp		
5111						565				570			575					
E-->	5113	aaa	ctg	ccc	cct	gtc	ccc	tct	agc	cgc	ctt	gga	gac	tca	tgg	ctg	ccc	1776
5114	Lys	Leu	Pro	Pro	Val	Pro	Ser	Ser	Arg	Leu	Gly	Asp	Ser	Trp	Leu	Pro		
5115						580				585			590					
E-->	5117	cgg	cca	atc	ccc	aaa	gta	cca	gta	tct	gcc	cca	agt	tcc	agt	gat	ccc	1824
5118	Arg	Pro	Ile	Pro	Lys	Val	Pro	Val	Ser	Ala	Pro	Ser	Ser	Ser	Asp	Pro		
5119						595				600			605					
E-->	5121	tgg	aca	gga	aga	gaa	tta	acc	aac	cg	cac	tca	ctt	cca	ttt	tca	ttg	1872
5122	Trp	Thr	Gly	Arg	Glu	Leu	Thr	Asn	Arg	His	Ser	Leu	Pro	Phe	Ser	Leu		

Same errors

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

5123	610	615	620																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
E--> 5125 ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
5126	Pro	Ser	Gln	Met	5125	610	615	620	1920																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
5126	Pro	Arg	Pro	Asp	Val	Pro	Arg	Leu	Gly	Ser	Thr																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
5127	625	630	635	640																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
E--> 5129 ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
5129	Phe	Ser	Leu	Asp	Thr	Ser	Met	Ser	Met	Asn	Ser	Ser	Pro	Leu	Val	Gly	1968																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005
TIME: 11:17:05

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272005\J539105.raw

E--> 5189 gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt 2688
5190 Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
5191 885 890 895
E--> 5193 tcc att tct tct cct gcc cat gta gct acc tag 2721
5194 Ser Ile Ser Ser Pro Ala His Val Ala Thr 2719
E--> 5195 900 905

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

10/539,105-

Page 6

<210> 4

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

✓ p/s see item #10
on error summary
sheet
INVALID
Response

<400> 4

cgtgaagaag agctctgggt t

21

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/27/2005
PATENT APPLICATION: US/10/539,105 TIME: 11:17:06

Input Set : A:\PTO.RJ.txt
Output Set : N:\CRF4\06272005\J539105.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005

TIME: 11:17:06

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3988 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:247,Line#:3984
L:4478 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:249,Line#:4474
L:4968 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:251,Line#:4964
L:4985 M:254 E: No. of Bases conflict, LENGTH:Input:240 Counted:238 SEQ:251 ✓
L:4986 M:351 W: Sequence data Name/Key Feature' Out-of-Range, SEQ ID#: 251, CDS
LOCATION:1..2718
M:254 Repeated in SeqNo=251
L:5195 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2721 Found:2719 SEQ:251 ✓
L:5458 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:253,Line#:5454
L:5948 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:255,Line#:5944
L:6438 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:257,Line#:6434
L:6928 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:259,Line#:6924